MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR
PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA
LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH

FIG. I

TCCGCAGGCGGACCGGGGGCAAAGGAGGTGGCATGTCGGTCAGGCACAGCAGGGTCCTGT
GTCCGCGCTGAGCCGCGCTCTCCCTGCTCCAGCAAGGACC
><Met (trans-1-s, dir=f, res-1}>
ATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGTGCCTGGTGTTGGCGCTGCCTGCC
CTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTACCCCTGGCGGGAC
GCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGG
CCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
TTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAG
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTC
GCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC
CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCC
AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC
CTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC
CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT
TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAG
GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGG
CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTG
CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC
TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCCACTTGCACTGAAAGAGG
CTTTTTTTTAAATAAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

FIG. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
GAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT

FIG. 3

```
SEQ ID NO:4   128  GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
SEQ ID NO:5     1  GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACG
SEQ ID NO:6     1                                                   G
SEQ ID NO:3     1  GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG

SEQ ID NO:4   178  CA-TTCTGGAACTACCTGGAGCGC
SEQ ID NO:5    51  CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG
SEQ ID NO:6     2  CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG
SEQ ID NO:3    51  CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG

SEQ ID NO:5   101  GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGCGCCT
SEQ ID NO:6    52  GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
SEQ ID NO:7     1            GAGGGGCCCCCAGGAGTGGTGGCCGGAGGTG
SEQ ID NO:3   101  GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT

SEQ ID NO:5   151  GCNGCTGCAGCACCGGNTTCTTCGCGCACGCTGNTTTCTGCTTGGAGCAC
SEQ ID NO:6   102  GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
SEQ ID NO:7    32  TGGCAGGGGTCAGGTTGCTGGTCCCAGCCTTGCACCCTGAGCTAGGACAC
SEQ ID NO:3   151  GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC

SEQ ID NO:5   201  GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA
SEQ ID NO:6   152  GCATCGTGTCCACCTGGTGCCGGCGTGATTNCCCCGGGCACCCCCAGCCA
SEQ ID NO:7    82  CAGTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
SEQ ID NO:8     1  GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
SEQ ID NO:10    1      CTTGTCCACCTGGTGCCGGCGTGATTNCCC-GGGCACCCCCAGCCA
SEQ ID NO:3   201  GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA

SEQ ID NO:5   251  GAACACGCA-TGCAAAGCCGTG
SEQ ID NO:7   132  GAACACGCAGN-CC-AGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO:8    51  GAACACGCAG-GCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO:10   47  GAACACGCAGTGCC-AGCCNT-CCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO:9     1          AGCNGTGCNCCNCAGGCACCTTCTCAGCCAGCAGT
SEQ ID NO:3   251  GAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC

SEQ ID NO:7   182  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO:8   101  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO:10   97  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCAACGCCCTGGNC-T
SEQ ID NO:9    36  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO:3   301  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT

SEQ ID NO:7   232  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAG
SEQ ID NO:8   151  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO:10  147  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO:9    86  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACGCTGTGCACCAGCT
SEQ ID NO:3   351  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT

SEQ ID NO:10  197  GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
SEQ ID NO:9   136  GCACTGGCTTCCCCCTCAGCACCAGGGTANCAGGAGCTGAGGAGTGTGAG
SEQ ID NO:3   401  GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG

SEQ ID NO:10  247  CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO:9   186  CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO:3   451  CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
```

FIG. 4

FIG. 5

```
DNA30942    1    MRALEGPGLSLCLVLALPALPVPAVRGVAETPTYPWRD.AETG
hTNFR2      1    MAPVAVWAALAVGLELWAAAHALPAQVAFTPV.APEPGSTCRLREYYDQT
                                                        CRD 1

DNA30942   45    ERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLRRCRYCNVL
hTNFR2     50    AQMCCSKCSPGQHAKVPCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR
                                              CRD 2

DNA30942   95    CGEREEEARACHATHNRACRCRTGFF..AHAG.FCLEHASCPPGAGV
hTNFR2    100    CSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGV
                      CRD 2                                CRD 3

DNA30942  139    IAPGTPSQNTQCQPCPPGTFSASSSSEQCQPHRNCTALGLALNVPGSS
hTNFR2    150    ARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVA...IPGNAS
                   CRD 3                                    CRD 4

DNA30942  189    HDTLCTSCTGFPLSTRVPGABECERAVIDFVAFQDISIKRLLQRLLQALEA
hTNFR2    196    RDAVCTSTS..PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLL
                                     CRD 4

DNA30942  239    PEGWGPTP..RAGRAALQLKRRLTELGADQDGALLVRLLQALRVARMP.
hTNFR2    244    PMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPL

DNA30942  287    GLERSVRERFLPVH
hTNFR2    293    CLLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRA

hTNFR2    343    PTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD

hTNFR2    393    HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLG

hTNFR2    443    ETEEKPLPLGVPDAGMKPS
```

```
DcR3   1 MRALEGPGLSLCLVLALPALLPVPAVRGVA  31
OPG    1 MNKLLCCALVFLDLSIKWTTQETFP-----  25

                              CRD1
DcR3  32 ETPTYPWRDAETGERLVCAQCPPGTPVQRPC  62
OPG   26 PK-YLHYDEETSHQLLCDKCPPGTYLKQHC   54

DcR3  63 RRDSPTTCGPCPPRHYTQFWNYLERCRYCNV  93
OPG   55 TAKWKTVCAPCPDHYYTDSWHTSDECLYCSP  85

                         CRD2
DcR3  94 LCGREEEARACHATHNRACRCRTGFFAHAG  124
OPG   86 VCKELQYVKQECNRTHNRVCECKEGRYLEIR 116

                      CRD3
DcR3 125 FCLEHASCPPGAGVIAPGTPSQNTQCPP    155
OPG  117 FCLKHRSCPPGFGVVQAGTPERNTVCKRCPD 147

                  CRD4
DcR3 156 GTFSASSSEQCQPHRNCTALGLALNVPGS   186
OPG  148 GFFSNETSSKAPCRKHTNCSVFGLLLTQKGN 178

DcR3 187 SSHDTLCTSCTGFPLSTRVPGABECERAVID 217
OPG  179 ATHDNICSGNSESTQKCGID-VTLCEEAFFR 208

DcR3 218 FVAFQDISIKRLQRLLQALEAPEGWGPT-PR 247
OPG  209 FAVPPTXFTPNWLSVLVDNLPGTKVNAESVER 239

DcR3 248 AGRAALQLKLRRRTELLGAQDGAL-LVRLL  277
OPG  240 IKRQHSSQEQTFQLLKLWKHQNKAQDIVKKI 270

DcR3 278 QALRVARMPGLERSVRRRFLPVH         300
OPG  271 IQDIDLCENSVQRHIGHANLTFE         293...
```

FIG.6
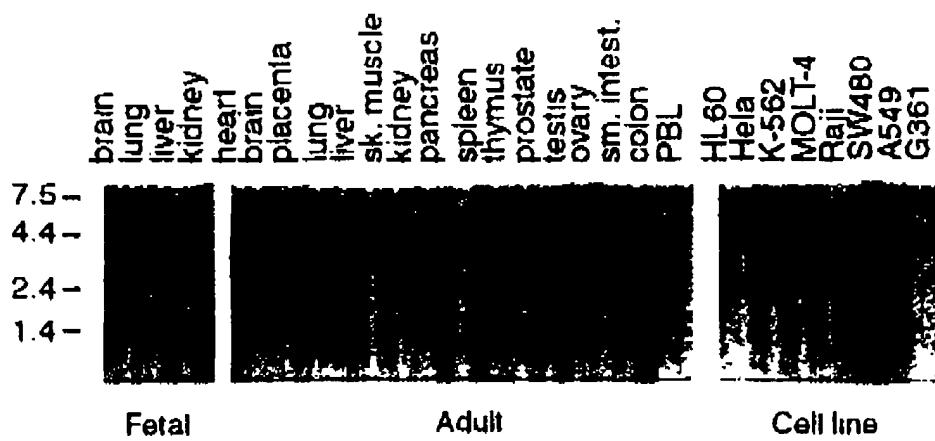
FIG. 7
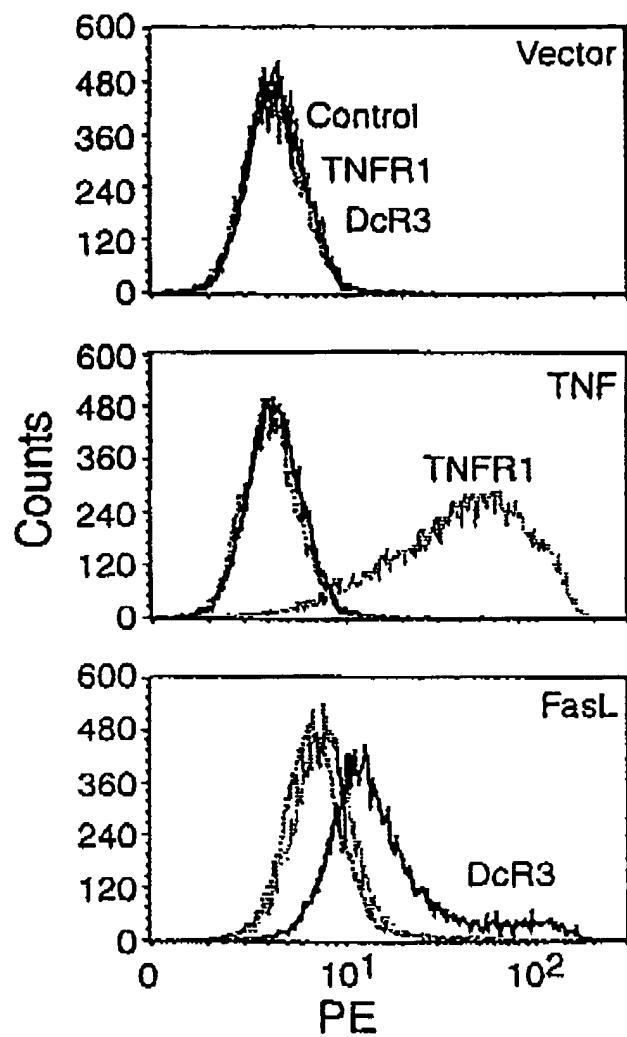
FIG. 8A
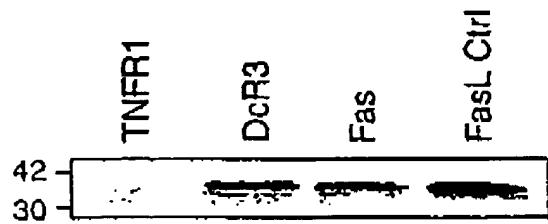
FIG. 8B
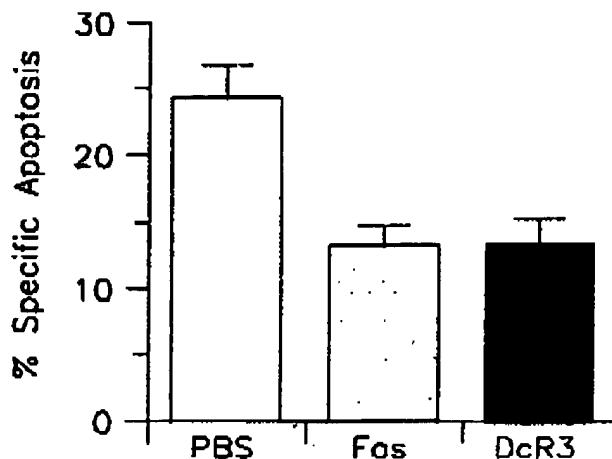
FIG. 9A
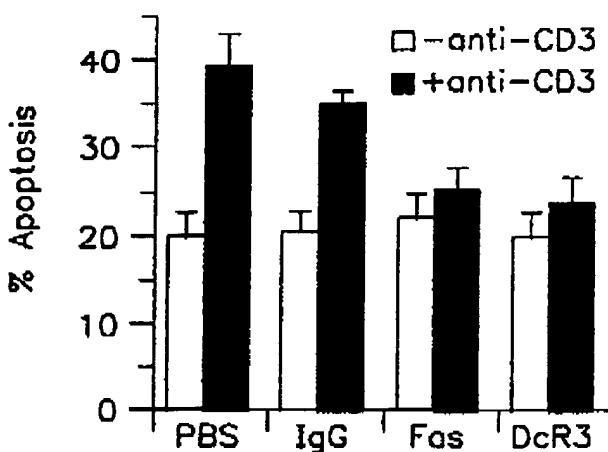
FIG. 9B
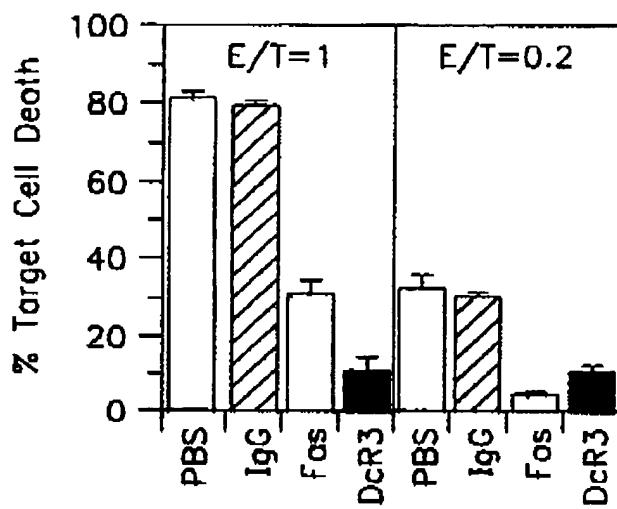
FIG. 9C
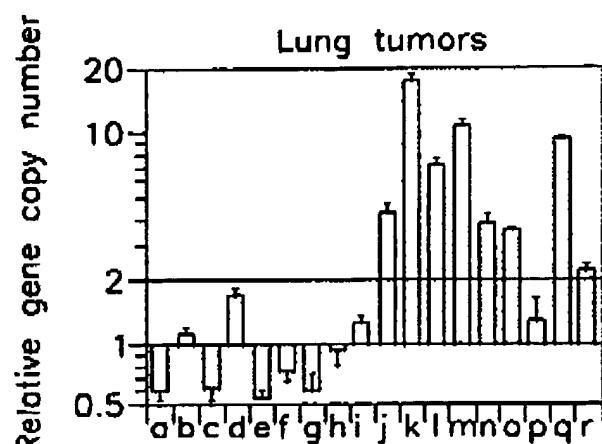
FIG. IOA
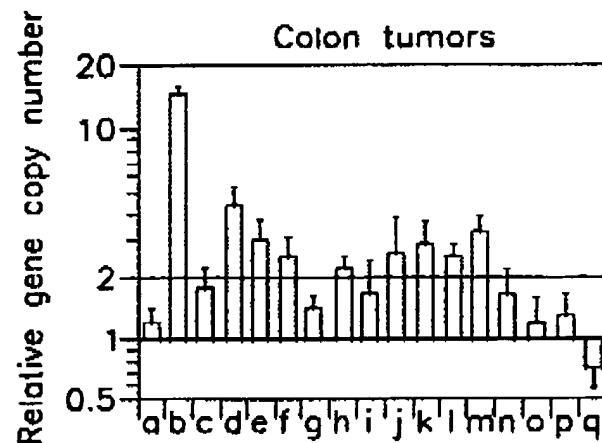
FIG. IOB

FIG. IOC

FIG. IOD

Human MLR

FIG. I IA

Murine MLR

FIG. I IB
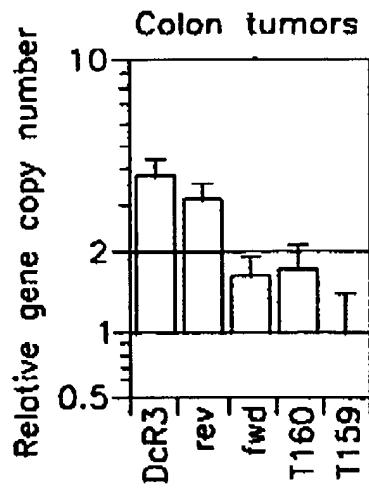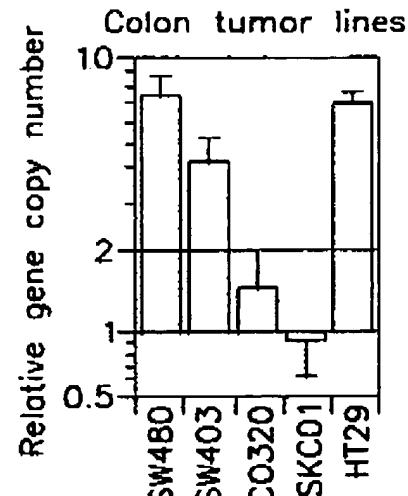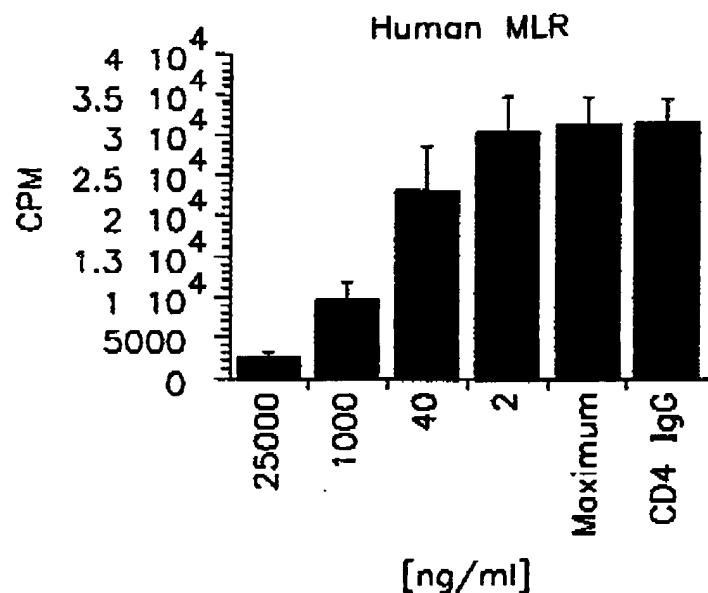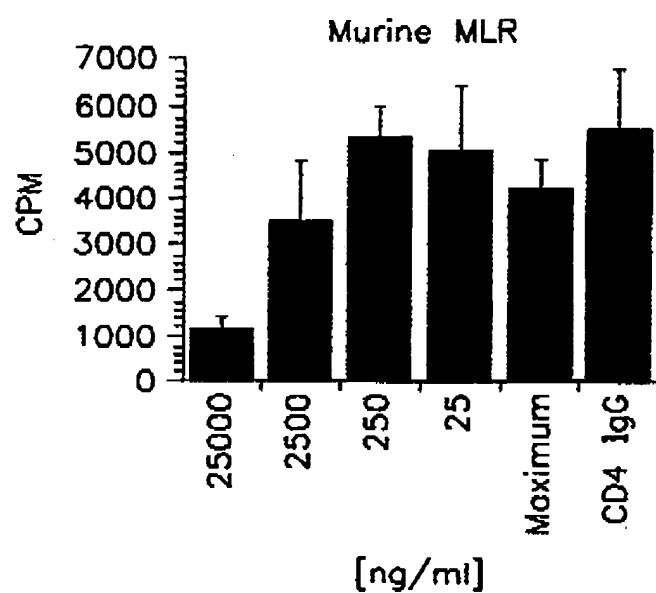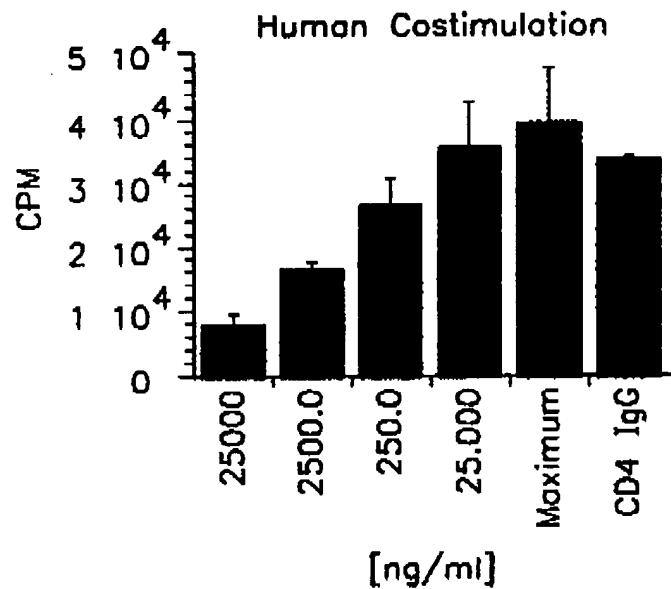
FIG. 11C

mAb	Isotype	Antigen Specificity (ELISA)					% Blocking (ELISA)
		DCR3	DR4	DR5	DcR1	OPG	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.
% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

FIG. 12

FIG. 13

FIG. 14